FASTA searches a protein or DNA sequence data bank
 version 3.3t05 March 30, 2000
 Please cite:
 W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

/tmp/fastaCAACZaWfX: 1219 aa
 >SEQ ID NO 23 human transporter
 vs   /tmp/fastaDAADZaWfX library
searching /tmp/fastaDAADZaWfX library

    1382 residues in 1 sequences

FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 2
 join: 40, opt: 28, gap-pen: -12/ -2, width: 16
 Scan time: 0.050
The best scores are: opt
gi|21729873|ref|NP_115972.2| ATP-binding cassette   (1382) 4838

>>gi|21729873|ref|NP_115972.2| ATP-binding cassette, sub   (1382 aa)
 initn: 7928 init1: 4838 opt: 4838
Smith-Waterman score: 7606; 88.061% identity in 1382 aa overlap (1-1219:1-1382)

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                10        20        30        40        50        60
SEQ    MTRKRTYWVPNSSGGLVNRGIDIGDDMVSGLIYKTYTLQDGPWSQQERNPEAPGRAAVPP
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|217 MTRKRTYWVPNSSGGLVNRGIDIGDDMVSGLIYKTYTLQDGPWSQQERNPEAPGRAAVPP
                10        20        30        40        50        60

                70        80        90       100       110       120
SEQ    WGKYDAALRTMIPFRPKPRFPAPQPLDNAGLFSYLTVSWLTPLMIQSLRSRLDENTIPPL
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|217 WGKYDAALRTMIPFRPKPRFPAPQPLDNAGLFSYLTVSWLTPLMIQSLRSRLDENTIPPL
                70        80        90       100       110       120

               130       140       150       160       170       180
SEQ    SVHDASDKNVQRLHRLWEEEVSRRGIEKASVLLVMLRFQRTRLIFDALLGICFCIASVLG
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|217 SVHDASDKNVQRLHRLWEEEVSRRGIEKASVLLVMLRFQRTRLIFDALLGICFCIASVLG
               130       140       150       160       170       180

               190       200       210       220       230       240
SEQ    PILIIPKILEYSEEQLGNVVHGVGLCFALFLSECVKSLSFSSSWIINQRTAIRFQAAVSS
       :::::::::::::::::::::::::::::::::::::::::::::::::::::::::: ::::
gi|217 PILIIPKILEYSEEQLGNVVHGVGLCFALFLSECVKSLSFSSSWIINQRTAIRFRAAVSS
               190       200       210       220       230       240

               250       260       270       280       290       300
SEQ    FAFEKLIQFKSVIHITSGEAISFFTGDVNYLFEGVCYGPLVLITCASLVICSISSYFIIG
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|217 FAFEKLIQFKSVIHITSGEAISFFTGDVNYLFEGVCYGPLVLITCASLVICSISSYFIIG
               250       260       270       280       290       300

               310       320       330       340       350       360
SEQ    YTAFIAILCYLLVFPLEVFMTRMAVKAQHHTSEVSDQRIRVTSEVLTCIKLIKMYTWEKP
       :::::::::::::::::::::: :::::::::::::::::::::::::::::::::::::::
gi|217 YTAFIAILCYLLVFPLAVFMTRMAVKAQHHTSEVSDQRIRVTSEVLTCIKLIKMYTWEKP
               310       320       330       340       350       360

               370       380       390       400       410       420
SEQ    FAKIIEDLRRKERKLLEKCGLVQSLTSITLFIIPTVATAVWVLIHTSLKLKLTASMAFSM
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|217 FAKIIEDLRRKERKLLEKCGLVQSLTSITLFIIPTVATAVWVLIHTSLKLKLTASMAFSM
               370       380       390       400       410       420
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              430       440       450       460       470       480
SEQ    LASLNLLRLSVFFVPIAVKGLTNSKSAVMRFKKFFLQESPVFYVQTLQDPSKALVFEEAT
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|217 LASLNLLRLSVFFVPIAVKGLTNSKSAVMRFKKFFLQESPVFYVQTLQDPSKALVFEEAT
              430       440       450       460       470       480

              490       500       510       520       530       540
SEQ    LSWQQTCPGIVNGALELERNGHASEGMTRPRDALGPEEEGNSLGPELHKINLVVSKGMML
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|217 LSWQQTCPGIVNGALELERNGHASEGMTRPRDALGPEEEGNSLGPELHKINLVVSKGMML
              490       500       510       520       530       540

              550       560       570       580       590       600
SEQ    GVCGNTGSGKSSLLSAILEEMHLLEGSVGVQGSLAYVPQQAWIVSGNIRENILMGGAYDK
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|217 GVCGNTGSGKSSLLSAILEEMHLLEGSVGVQGSLAYVPQQAWIVSGNIRENILMGGAYDK
              550       560       570       580       590       600

              610       620       630       640       650       660
SEQ    ARYLQVLHCCSLNRDLELLPFGDMTEIGERGLNLSGGQKQRISLARAVYSDRQIYLLDDP
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|217 ARYLQVLHCCSLNRDLELLPFGDMTEIGERGLNLSGGQKQRISLARAVYSDRQIYLLDDP
              610       620       630       640       650       660

              670       680       690       700       710       720
SEQ    LSAVDAHVGKHIFEECIKKTLRGKTVVLVTHQLQYLEFCGQIILLENGKICENGTHSELM
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|217 LSAVDAHVGKHIFEECIKKTLRGKTVVLVTHQLQYLEFCGQIILLENGKICENGTHSELM
              670       680       690       700       710       720

              730
SEQ    QKKGKYAQLIQKMHKEATS------------------------------------------
       :::::::::::::::::::::
gi|217 QKKGKYAQLIQKMHKEATSDMLQDTAKIAEKPKVESQALATSLEESLNGNAVPEHQLTQE
              730       740       750       760       770       780


SEQ    ------------------------------------------------------------
gi|217 EEMEEGSLSWRVYHHYIQAAGGYMVSCIIFFFVVLIVFLTIFSFWWLSYWLEQGSGTNSS
              790       800       810       820       830       840


SEQ    ------------------------------------------------------------
gi|217 RESNGTMADLGNIADNPQLSFYQLVYGLNALLLICVGVCSSGIFTKVTRKASTALHNKLF
              850       860       870       880       890       900

       740       750       760       770       780       790
SEQ    --VFRCPMSFFDTIPIGRLLNCFAGDLEQLDQLLPIFSEQFLVLSLMVIAVLLIVSVLSP
         ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|217 NKVFRCPMSFFDTIPIGRLLNCFAGDLEQLDQLLPIFSEQFLVLSLMVIAVLLIVSVLSP
              910       920       930       940       950       960

       800       810       820       830       840       850
SEQ    YILLMGAIIMVICFIYYMMFKKAIGVFKRLENYSRSPLFSHILNSLQGLSSIHVYGKTED
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|217 YILLMGAIIMVICFIYYMMFKKAIGVFKRLENYSRSPLFSHILNSLQGLSSIHVYGKTED
              970       980       990      1000      1010      1020
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          860       870       880       890       900       910
SEQ     FISQFKRLTDAQNNYLLLFLSSTRWMALRLEIMTNLVTLAVALFVAFGISSTPYSFKVMA
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|217  FISQFKRLTDAQNNYLLLFLSSTRWMALRLEIMTNLVTLAVALFVAFGISSTPYSFKVMA
          1030      1040      1050      1060      1070      1080

          920       930       940       950       960       970
SEQ     VNIVLQLASSFQATARIGLETEAQFTAVERILQYMKMCVSEAPLHMEGTSCPQGWPQHGE
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|217  VNIVLQLASSFQATARIGLETEAQFTAVERILQYMKMCVSEAPLHMEGTSCPQGWPQHGE
          1090      1100      1110      1120      1130      1140

          980       990       1000      1010      1020      1030
SEQ     IIFQDYHMKYRDNTPTVLHGINLTIRGHEVVGIVGRTGSGKSSLGMALFRLVEPMAGRIL
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|217  IIFQDYHMKYRDNTPTVLHGINLTIRGHEVVGIVGRTGSGKSSLGMALFRLVEPMAGRIL
          1150      1160      1170      1180      1190      1200

          1040      1050      1060      1070      1080      1090
SEQ     IDGVDICSIGLEDLRSKLSVIPQDPVLLSGTIRFNLDPFDRHTDQQIWDALERTFLTKAI
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|217  IDGVDICSIGLEDLRSKLSVIPQDPVLLSGTIRFNLDPFDRHTDQQIWDALERTFLTKAI
          1210      1220      1230      1240      1250      1260

          1100      1110      1120      1130      1140      1150
SEQ     SKFPKKLHTDVVENGGNFSVGERQLLCIARAVLRNSKIILIDEATASIDMETDTLIQRTI
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|217  SKFPKKLHTDVVENGGNFSVGERQLLCIARAVLRNSKIILIDEATASIDMETDTLIQRTI
          1270      1280      1290      1300      1310      1320

          1160      1170      1180      1190      1200      1210
SEQ     REAFQGCTVLVIAHRVTTVLNCDHILVMGNGKVVEFDRPEVLRKKPGSLFAALMATATSS
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|217  REAFQGCTVLVIAHRVTTVLNCDHILVMGNGKVVEFDRPEVLRKKPGSLFAALMATATSS
          1330      1340      1350      1360      1370      1380


SEQ     LR
        ::
gi|217  LR



1219 residues in 1 query    sequences
1382 residues in 1 library sequences
 Scomplib [version 3.3t05 March 30, 2000]
 start: Mon Nov 11 10:23:05 2002 done: Mon Nov 11 10:23:06 2002
 Scan time:  0.050 Display time:  2.400

Function used was FASTA
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